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TAGGCATAAATTGGTCTGCGCACCAGCACCATGCAACTTTTTTCACCTCTGCCTAATCATC
1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
a ATCCGTATTTAACCAGACGCGTGGTCTGTTGAAAAAGTGGAGACGGATTAGTAG
  * A * I G L R T S T M Q L F H L C L I I -
  TCTTGTTTCATGCTCTACTGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATG
61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
a AGAACAAGTACAGGATGACAAGTTCGGAGGTTGACACGGAACCCACCGAAACCCCGTAC
  S C S C P T V Q A S K L C L G W L W G M -
  GACATCGACCCTTATAAAGAATTTGGAGCTACTGTGGAGTTACTCTCGTTTTTGCCTTCT
121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
a CTGTAGCTGGGAATATTTCTTAAACCTCGATGACACCTCAATGAGAGCAAAAACGGAAGA
  D I D P Y K E F G A T V E L L S F L P S -
  GACTTCTTTCTTTCAGTACGAGATCTTCTAGATACCGCCTCAGCTCTGTATCGGGAAGCC
181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
a CTGAAGAAAGGAAGTCATGCTCTAGAAGATCTATGGCGGAGTCGAGACATAGCCCTTCGG
  D F F P S V R D L L D T A S A L Y R E A * -
  TTAGAGTCTCCTGAGCATTGTTCACTCACCATACTGCACTCAGGCAAGCAATTCTTTGC
241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
a AATCTCAGAGGACTCGTAACAAGTGGAGTGGTATGACGTGAGTCCGTTTCGTTAAGAAACG
  L E S P E H C S P H H T A L R Q A I L C -
  TGGGGGGAATAATGACTCTAGCTACCTGGGTGGGTGTTAATTTGGAAGATCCAGCGTCT
301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
a ACCCCCCCTTGATTACTGAGATCGATGGACCCACCCACAATTAACCTTCTAGGTCGCAGA
  W G E L M T L A T W V G V N L E D P A S -
  AGAGACCTAGTAGTCAGTTATGTCAACACTAATATGGGCCTAAAGTTCAGGCAACTCTTG
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
a TCTCTGGATCATCAGTCAATACAGTTGTGATTATACCCGGATTTCAAGTCCGTTGAGAAC
  R D L V V S Y V N T N M G L K F R Q L L -
  TGGTTTCACATTTCTTGTCTCACTTTTGAAGAGAAACAGTTATAGAGTATTTGGTGTCT
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
a ACCAAAGTGTAAGAACAGAGTGAAAACCTTCTCTTTGTCAATATCTCATAAACACAGA
  W F H I S C L T F G R E T V I E Y L V S -
  TTCGGAGTGTGGATTTCGCACTCCTCCAGCTTATAGACCACCAAATGCCCCTATCCTATCA
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
a AAGCCTCACACCTAAGCGTGAGGAGGTCGAATATCTGGTGGTTTACGGGGATAGGATAGT
  F G V W I R T P P A Y R P P N A P I L S -
  AACTTCCGGAGACTACTGTTGTTAGACGACGAGGCAGGTCCCCTAGAAGAAGAACTCCC
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
a TGTGAAGGCCTCTGATGACAACAATCTGCTGCTCCGTCAGGGGATCTTCTTCTTGAGGG
  T L P E T T V V R R R G R S P R R R T P -
  TCGCCTCGCAGACGAAGGTCTCAATCGCCGCTCGCAGAAGATCTCAATCTCGGGAATCT
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
a AGCGGAGCGTCTGCTTCCAGAGTTAGCGGCGCAGCGTCTTCTAGAGTTAGAGCCCTTAGA
  S P R R R R S Q S P R R R R S Q S R E S -
  CAATGTTAG
661 ----- 669
  GTTACAATC
a Q C * -

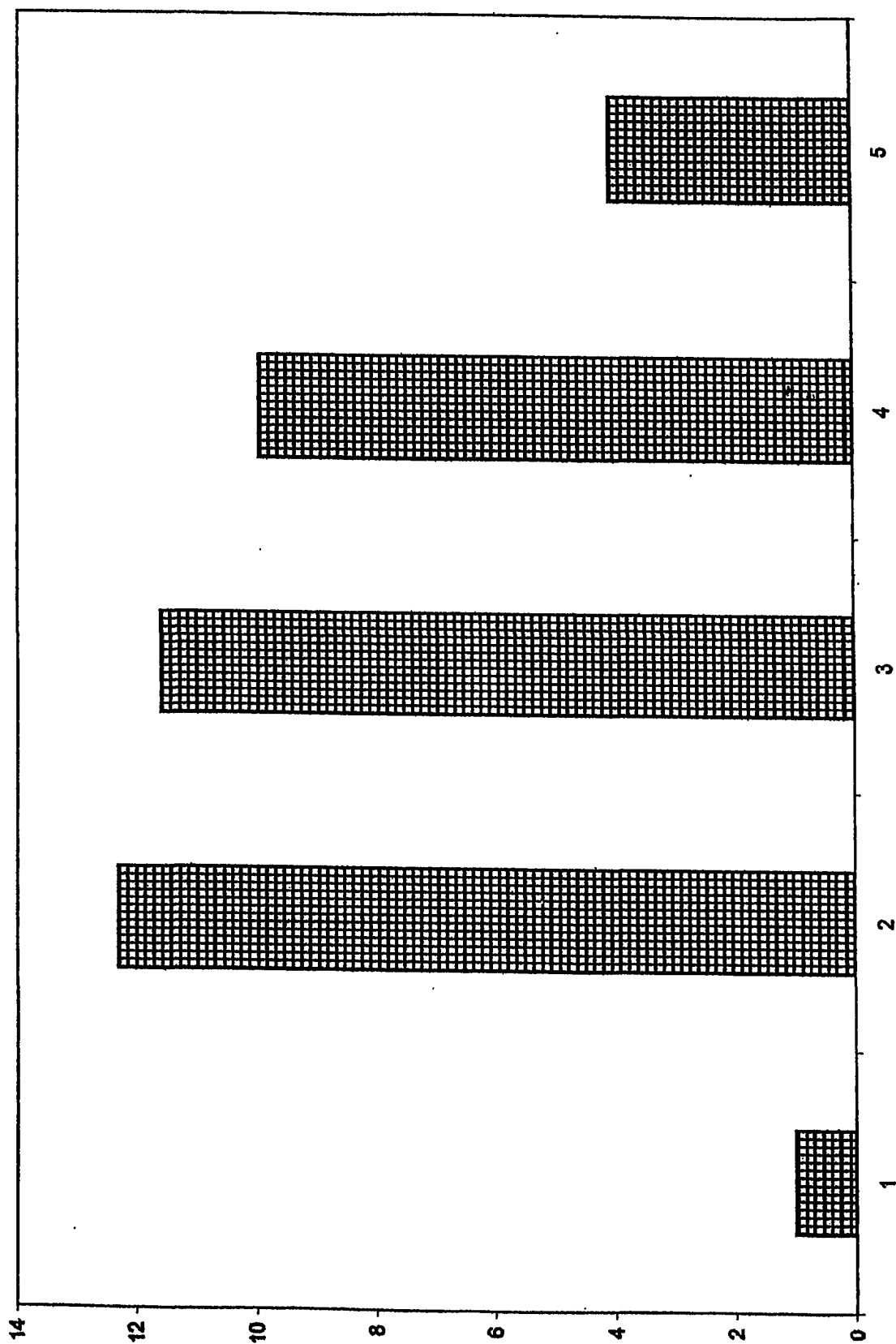
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Enzymes that do cut:

NONE

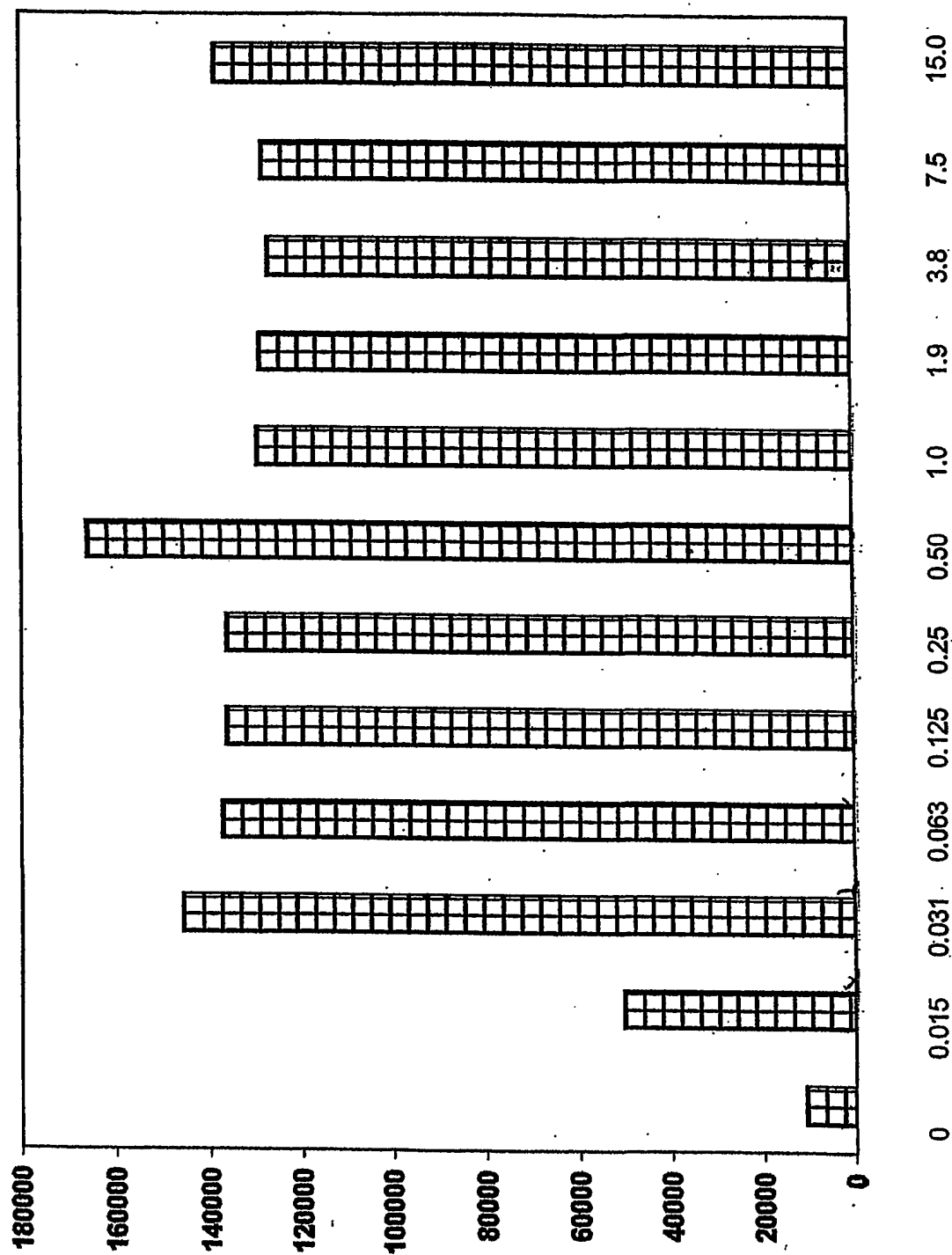
FIGURE 1

Figure 2



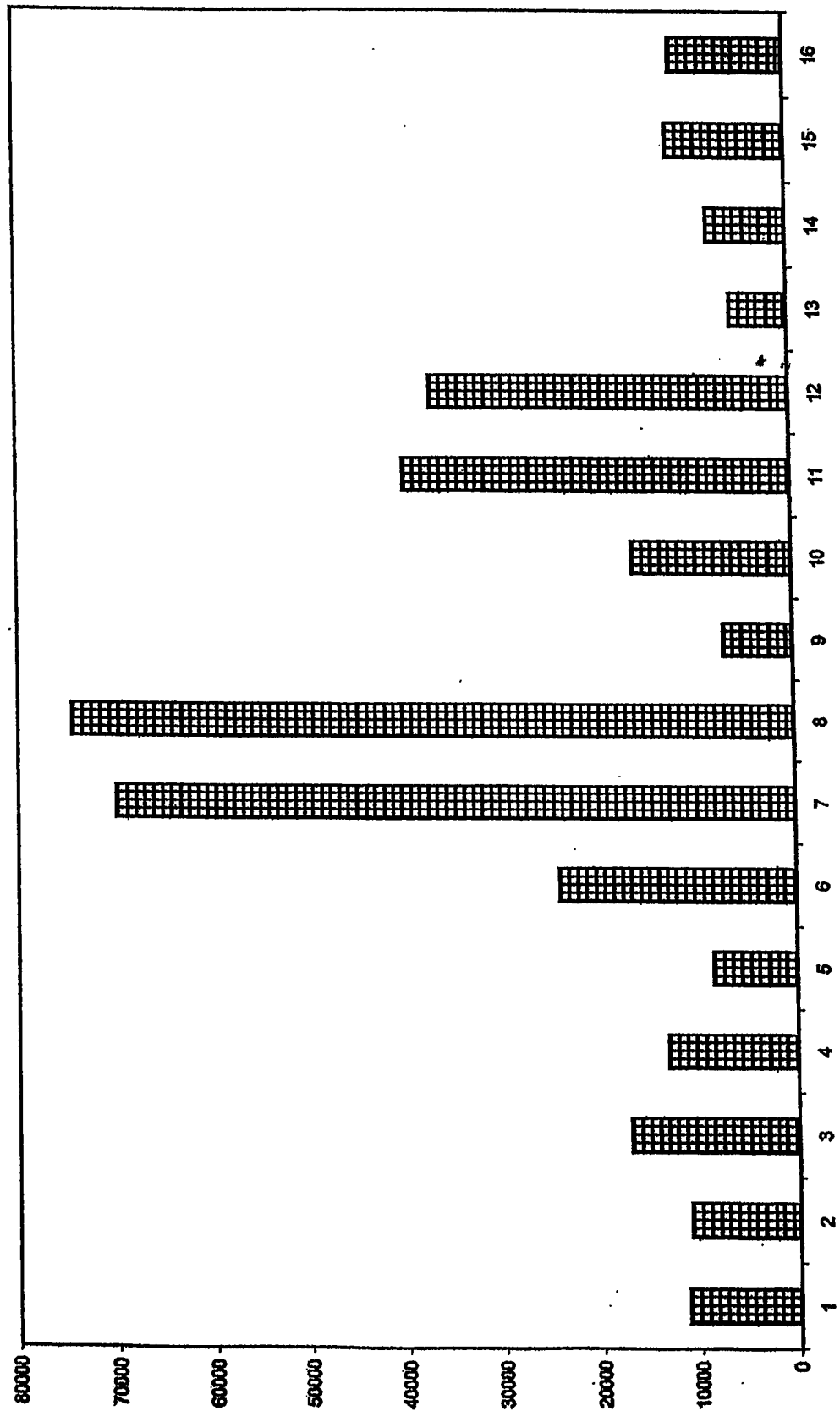
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Figure 3



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Figure 4a

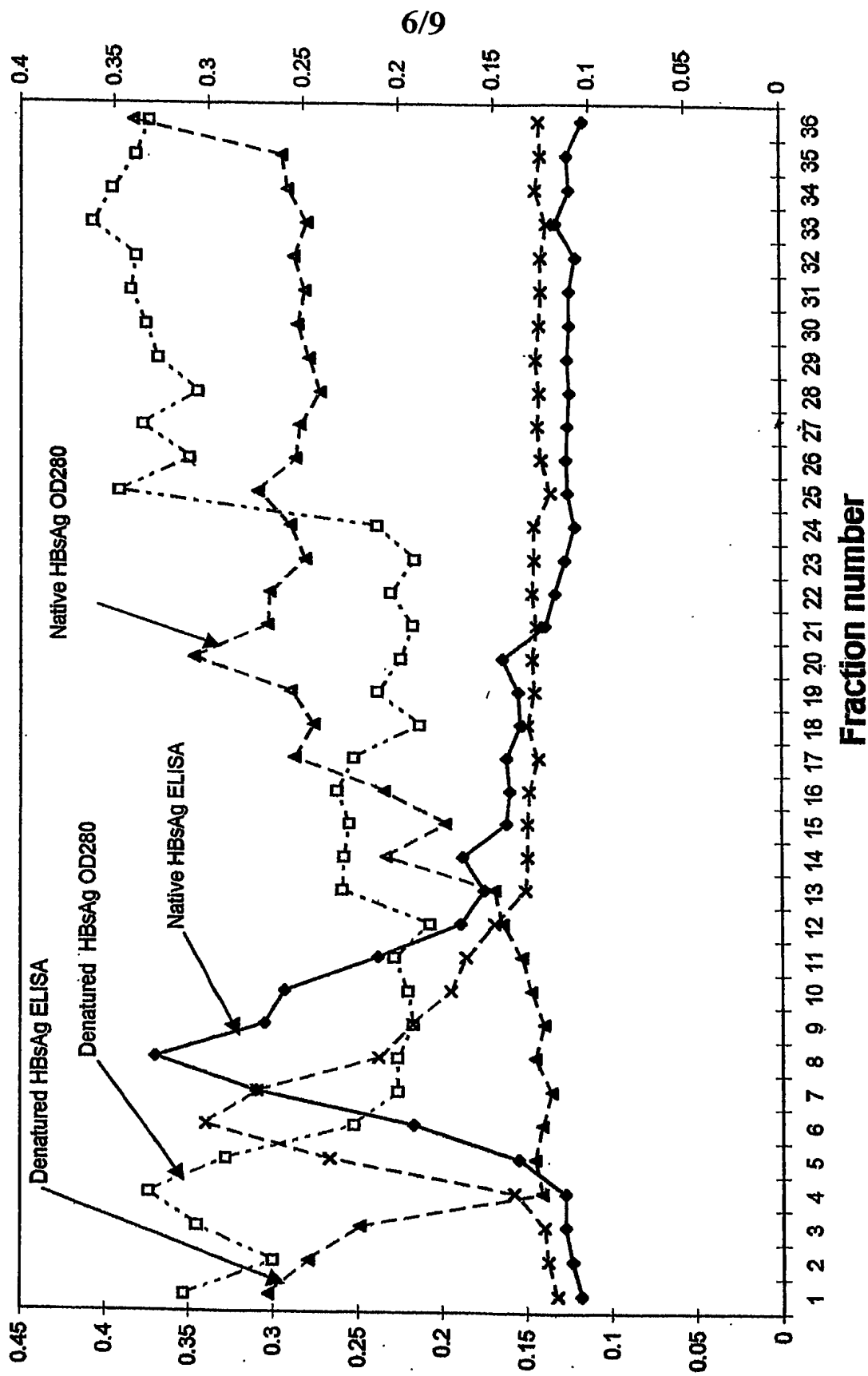


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Figure 4b

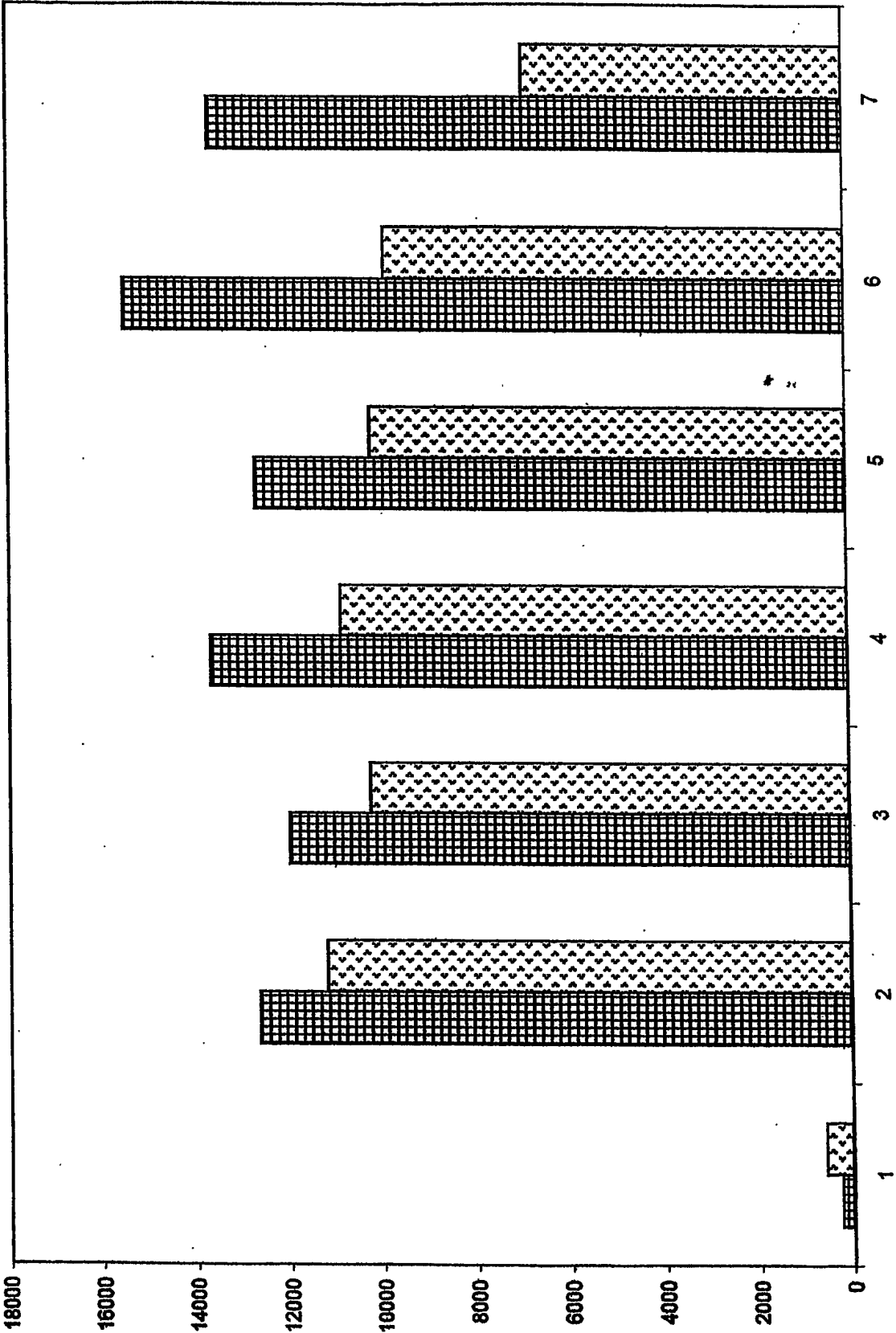
Treatment	day 2	day 3
Imm no ag	5096	11224
Imm 0.1 ug	5614	10904
Imm 1 ug	7266	16991
Imm 5 ug	5882	13120
Imm OT (3mg) no ag	4924	8409
Imm OT (3mg) 0.1 ug ag	7235	24250
Imm OT (3mg) 1 ug	14605	70078
Imm OT (3mg) 5 ag	11995	74585
Imm OT (1mg) no ag	3558	7079
Imm OT (1mg) 0.1 ug ag	4871	16339
Imm OT (1mg) 1 ug	4949	39954
Imm OT (1mg) 5 ag	4172	37059
Imm OT (0.1mg) no ag	5661	5904
Imm OT (0.1mg) 0.1 ug ag	12094	8168
Imm OT (0.1mg) 1 ug	23445	12242
Imm OT (0.1mg) 5 ag	36710	11754

Figure 5

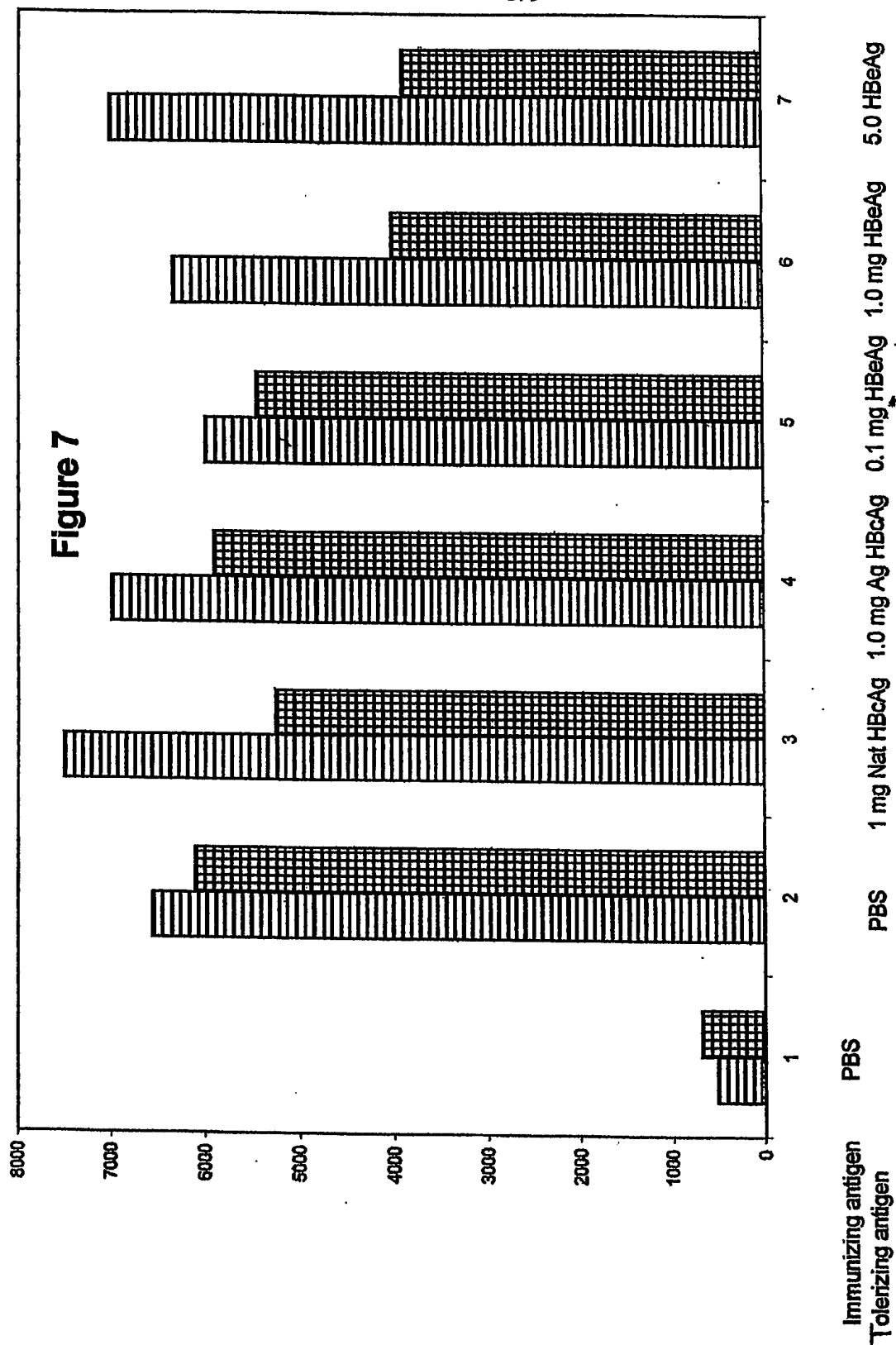


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Figure 6



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Figure 8

